# Searching Sequence Using HMM Profile (HMM3 Search)

The *HMM3 search* tool reads a HMM profile from a file and searches a sequence for significantly similar sequence matches.

The sequence must be selected in the *Project View* or there must be an active *Sequence View* window opened.
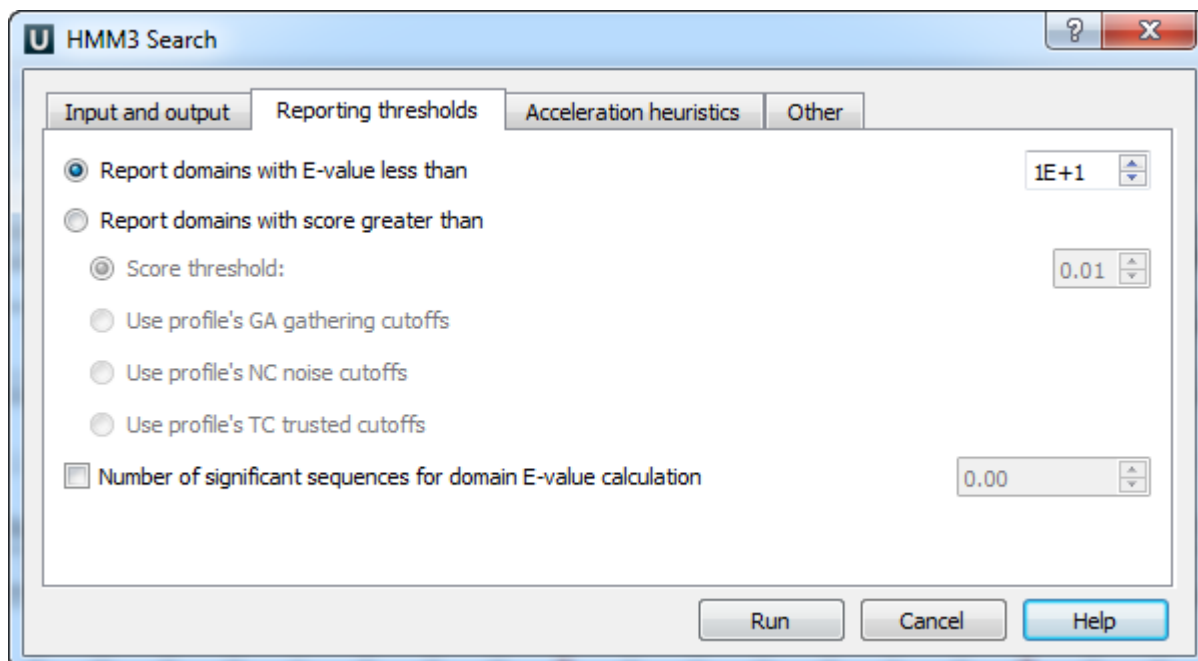
If the selected sequence is nucleic and profile HMM is built from amino alignment, the sequence will be automatically translated and searched in all possible frames (6 totally).

If a profile HMM is built for nucleic alignment, the search is performed for both strands (direct and complement).
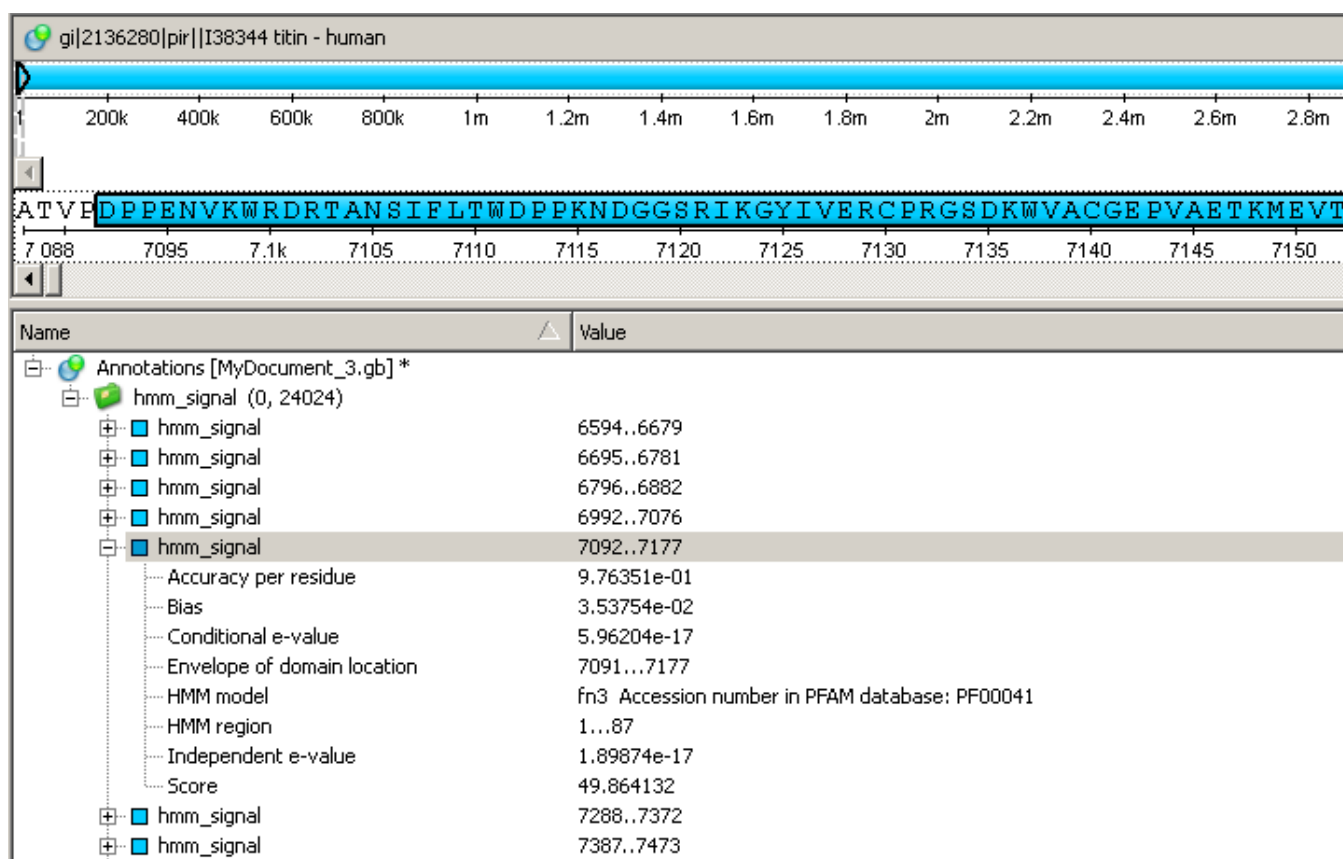
The *HMM3 search* accepts the HMMER2 HMM profiles (amino only) as a backward compatibility feature. An interesting post about using the HMMER2 models with the HMMER3 is available on the Sean Eddy's blog.
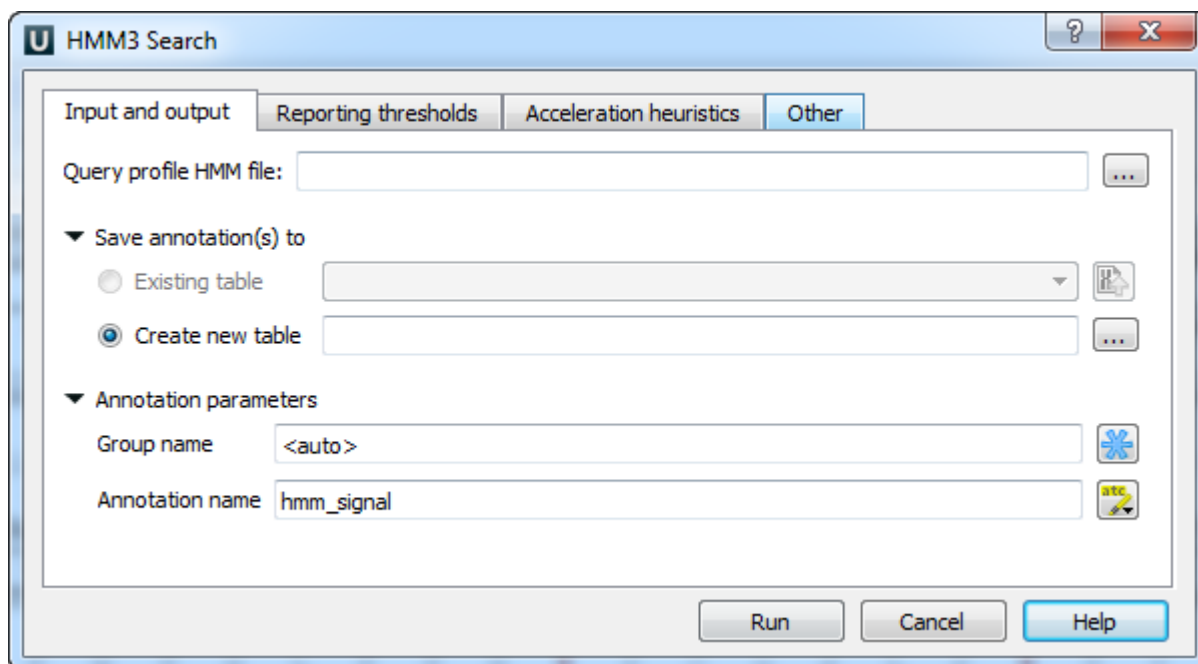
For example, reporting thresholds options can be configured using the dialog:

The search results are stored as sequence annotations in the Genbank file format.

gi|2136280|pir||I38344 titin - human

200k 400k 600k 800k 1m 1.2m 1.4m 1.6m 1.8m 2m 2.2m 2.4m 2.6m 2.8m

ATVP DPPENVKWRDRTANSIFLTWDPPKNDGGSRIKGYIVERCPRGSDKWVACGEPVAETKMEVT

7 088 7095 7.1k 7105 7110 7115 7120 7125 7130 7135 7140 7145 7150

Name	△	Value
Annotations [MyDocument_3.gb] *		
hmm_signal (0, 24024)		
hmm_signal		6594..6679
hmm_signal		6695..6781
hmm_signal		6796..6882
hmm_signal		6992..7076
hmm_signal		7092..7177
Accuracy per residue		9.76351e-01
Bias		3.53754e-02
Conditional e-value		5.96204e-17
Envelope of domain location		7091...7177
HMM model		fn3 Accession number in PFAM database: PF00041
HMM region		1...87
Independent e-value		1.89874e-17
Score		49.864132
hmm_signal		7288..7372
hmm_signal		7387..7473

The *HMM3 search* works only with files that contain a single HMM model.